

CLAIMS

1. An apparatus comprising:
 - a sequence database configured to contain entries of sequences;
 - a sequence comparator configured to receive a patient sample sequence, to compare the patient sample sequence with entries in the sequence database to determine closest matches, and to normalize a matching score of the closest matches.
2. The apparatus of claim A1, wherein the sequence comparator is further configured to determine whether the matching score of the closest matches are within a confidence threshold.
3. The apparatus of claim A2 further comprising:
 - a patient profile manager to reporting whether a sample patient identifier associated with the patient sample sequence matches a matched patient identifier associated with the closest match;
4. The apparatus of claim A3 wherein the patient sample sequence is sequenced from a virus.
5. The apparatus of claim A4 wherein the virus is hepatitis or Human Immunodeficiency Virus (HIV).
6. The apparatus of claim A3 wherein the patient sample sequence is sequenced from deoxyribonucleic acid (DNA).
7. The apparatus of claim A5 wherein the confidence threshold is approximately three standard deviations from an average normalized score.
8. A method comprising:

receiving a patient sample sequence, the patient sample sequence being associated with a sample patient identifier;

comparing the patient sample sequence with entries in a sequence database to determine closest matches, the closest matches being associated with a matched patient identifier;

normalizing a matching score of the closest matches.

9. The method of claim 8 further comprising:

determining whether the matching score of the closest matches are within a confidence threshold.

10. The method of claim 9 further comprising:

reporting the closest matches within the confidence threshold.

11. The method of claim 9 further comprising:

reporting whether the sample patient identifier matches the matched patient identifier;

12. The method of claim 11 wherein the patient sample sequence is sequenced from a virus.

13. The method of claim 12 wherein the virus is hepatitis or Human Immunodeficiency Virus (HIV).

14. The method of claim 10 wherein the patient sample sequence is sequenced from deoxyribonucleic acid (DNA).

15. The method of claim 13 wherein the confidence threshold is approximately three standard deviations from an average normalized score.

16. A computer-readable medium encoded with data and instructions, the data and instructions causing an apparatus executing the instructions to:

3 receive a patient sample sequence, the patient sample sequence being associated
4 with a sample patient identifier;
5 compare the patient sample sequence with entries in a sequence database to
6 determine closest matches, the closest matches being associated with a
7 matched patient identifier;
8 normalize a matching score of the closest matches.

1 17. The computer-readable medium of claim 16 wherein the instruction further
2 causes an apparatus to:
3 determine whether the matching score of the closest matches are within a
4 confidence threshold.

1 18. The computer-readable medium of claim 17 wherein the instruction further
2 causes an apparatus to:
3 report the closest matches within the confidence threshold.

1 19. The computer-readable medium of claim 18 wherein the instruction further
2 causes an apparatus to:
3 report whether the sample patient identifier matches the matched patient identifier;

1 20. The computer-readable medium of claim 19 wherein the patient sample
2 sequence is sequenced from a virus.

1 21. The computer-readable medium of claim 20 wherein the virus is hepatitis
2 or Human Immunodeficiency Virus (HIV).

1 22. The computer-readable medium of claim 18 wherein the patient sample
2 sequence is sequenced from deoxyribonucleic acid (DNA).

1 23. The computer-readable medium of claim 21 wherein the confidence
2 threshold is approximately three standard deviations from an average
3 normalized score.

1 24. An apparatus comprising:
2 means for receiving a patient sample sequence, the patient sample sequence being
3 associated with a sample patient identifier;
4 means for comparing the patient sample sequence with entries in a sequence
5 database to determine closest matches, the closest matches being
6 associated with a matched patient identifier;
7 means for normalizing a matching score of the closest matches.

1 25. The apparatus of claim 24 further comprising:
2 means for determining whether the matching score of the closest matches are
3 within a confidence threshold.

1 26. The apparatus of claim 25 further comprising:
2 means for reporting the closest matches within the confidence threshold.

1 27. The apparatus of claim 26 further comprising:
2 means for reporting whether the sample patient identifier matches the matched
3 patient identifier;

1 28. The apparatus of claim 27 wherein the patient sample sequence is
2 sequenced from a virus.

1 29. The apparatus of claim 28 wherein the virus is hepatitis or Human
2 Immunodeficiency Virus (HIV).

1 30. The apparatus of claim 26 wherein the patient sample sequence is
2 sequenced from deoxyribonucleic acid (DNA).

1 31. The apparatus of claim 29 wherein the confidence threshold is
2 approximately three standard deviations from an average normalized
3 score.